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Research Article

SeroWare: An Open-Source Software Suite for Voltammetry Data Acquisition and Analysis

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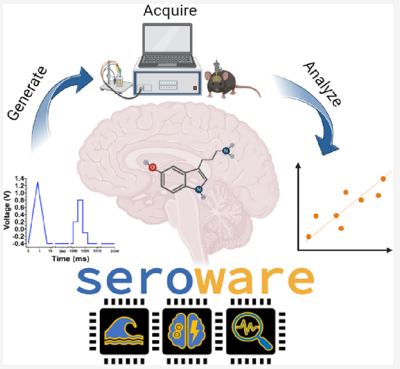
ABSTRACT: Voltammetry is widely used for fast, data-dense measurements of redox-active analytes in versatile environments, including the brain. Voltammetry requires minimal hardware beyond a potentiostat, a front-end amplifier, and a computer. Nonetheless, researchers must often develop or modify software packages for application-specific uses. Of the voltammetry software available, significant issues exist with source code inaccessible for updating or customization, nonconfigurable data processing procedures, and hardware incompatibilities. These limitations, coupled with the recent proliferation of waveform types and increased demands for high bandwidth data acquisition and efficient data processing, create the need for sophisticated, powerful, and flexible voltammetry software. We report developing "SeroWare", an open-source, end-to-end voltammetry acquisition and analysis software package designed to handle a wide variety of use cases encountered by voltammetry users. Although inspired by neurochemical analyses, this software is flexible, customizable, and compatible with open-source toolkits. The modular software architecture enables users to generate, acquire, and analyze voltammetry data of different types, ranging from pulse and sweep waveforms to fast and slow scans via easily accessible and exportable file formats. Template code is provided for communicating with a variety of standard external devices. We report several novel features for waveform applications and data flow. In-depth documentation in a User Guide and video tutorials are provided to enable new research directions, particularly regarding shareability and lowering the barriers to entry for new investigators.



KEYWORDS: *voltammetry, scientific software, electrochemistry, neurotransmitters, MATLAB*

1. INTRODUCTION

Fast voltammetry for neurochemical monitoring is in its fifth decade.[1] Advances in the field have focused on developing and implementing faster and longer measurements,[2,3] novel waveforms,[4−9] electrode materials and arrays,[10−12] and data processing techniques.[13−22] Over 12,000 publications on fast-scan cyclic voltammetry for neurotransmitter detection have been published in the past decade alone. The data acquisition and analysis software that measurements rely on supports these developments. Yet only a few published software packages provide the acquisition capabilities required for performing voltammetry for neurochemical analyses.[23−26]

Rapid increases in data acquisition speeds and storage capacities have enabled new voltammetry techniques and data analysis tools to extract maximal chemical information from voltammograms.[9,13,14,19,22,27−39] Yet, no single platform allows users to use these advances widely. Current open-source and commercial electroanalytical software focus on mechanistic simulations,[40] amenable only to slow scan methods or other niche applications,[41] or they aid in analyzing postacquisition data.[42] Most existing voltammetry software is costly, no longer maintained, poorly documented, or not freely available, forcing research groups to write time-consuming custom code solutions unavailable to others.

Meanwhile, neuroscience,[43] genetics,[44] bioinformatics,[45] and chemometrics[46] have benefited from a community-involved open-source software approach to data acquisition and analysis, including open-source data sets. Voltammetry would benefit similarly from readily available, easy-to-use, well-documented, and well-maintained software with end-to-end acquisition and analysis capabilities. This software would include everything needed to run a voltammetry experiment on the software side, from waveform generation to configuring and acquiring devices to processing and extracting data and performing machine learning for data analysis.

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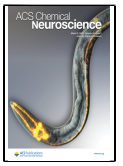

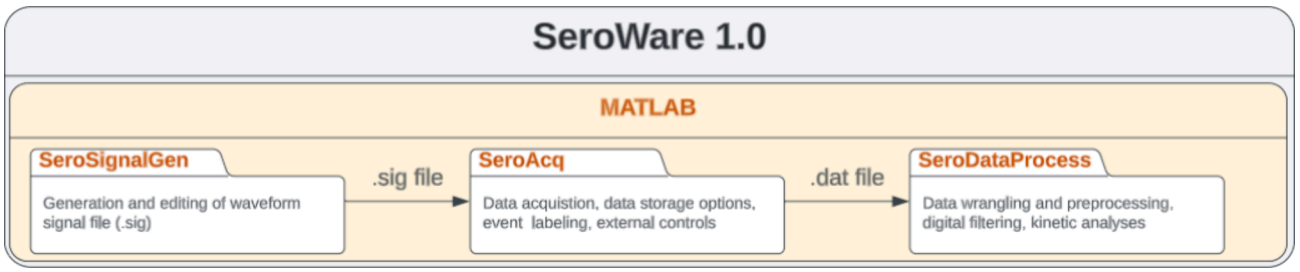

Figure 1. Overview of the SeroWare software suite.

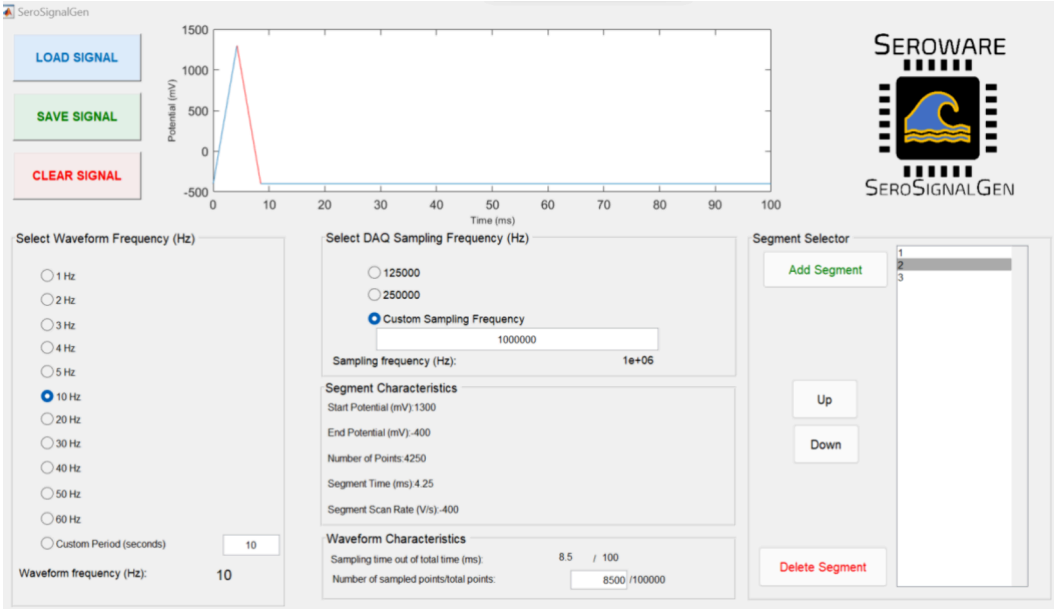

Figure 2. SeroSignalGen user interface, in which a triangle waveform was built in a segment-wise manner.

To fill these needs and move toward a community approach for voltammetry software, we wrote and released SeroWare (available at https://github.com/csmova/SeroWare), an acquisition and analysis software geared toward neurochemical analyses yet completely flexible for general use. While some of the most used voltammetry acquisition software is written in LabVIEW, we wrote the initial SeroWare version in MATLAB. MATLAB is one of the most commonly used academic and scientific software development languages.[47] It offers access to built-in graphical user interface (GUI) building, as well as data acquisition and analysis tools. Moreover, MATLAB is compatible with open-source domain-specific signal processing and data analysis scripts.[48−52] While LabVIEW is maintained by National Instruments (NI) and has facile NI card communication, MATLAB contains the built-in data acquisition (DAQ) toolbox as a powerful alternative. Further, MATLAB is optimized for vectorized data analyses, lending itself naturally to electrochemical data processing.

The shareability of new software is paramount. To compete with LabVIEW, which is free, we provide compiled versions of SeroWare that run in standalone mode where no MATLAB installation or license is required. A MATLAB license is needed to make custom edits to the codebase. This is commonly provided to researchers at academic institutions free of charge. The software is compatible with field-standard multifunction input/output (PCI) devices for potentiostat connections. We offer an "out of the box" compiled version and a developer/advanced user version for those who want to customize and incorporate their scripts into the codebase. All software versions are publicly available (https://github.com/csmova/SeroWare) with extensive documentation and tutorials on typical example use cases and information for users who want to customize the software for specialized needs. We encourage further testing, feature and issue requests, and code contributions through GitHub.

We named the software package SeroWare in honor of the fact that it was initially developed for brain serotonin monitoring via voltammetry. Nonetheless, SeroWare applies to the analysis of any electroactive analyte or any mode of voltammetry (e.g., chronoamperometry, sweep voltammetry, pulse voltammetry, *etc.*), including a wide variety of applications in the voltammetric electronic tongue field (*e.g.*, wastewater, food, beverage analyses).[53−56] We introduce several new features and unique data workflows not reported in previous software publications. These include a separate module for waveform generation that intuitively allows users to design, edit, and share a variety of waveforms and acquisition methods (FSCV, FSCAV, *etc.*), limited only by their choice of hardware. SeroWare enables real-time waveform modification, manual and automated external event labeling, and fully customizable data filtering, processing, and exporting modes. We also include working code to connect to and control standard auxiliary hardware devices (*e.g.*, injectors, stimulators, micromanipulators) over standard serial connections.

We previously published an *in vitro* and *in vivo* validation study using a pilot version of SeroWare that enabled data

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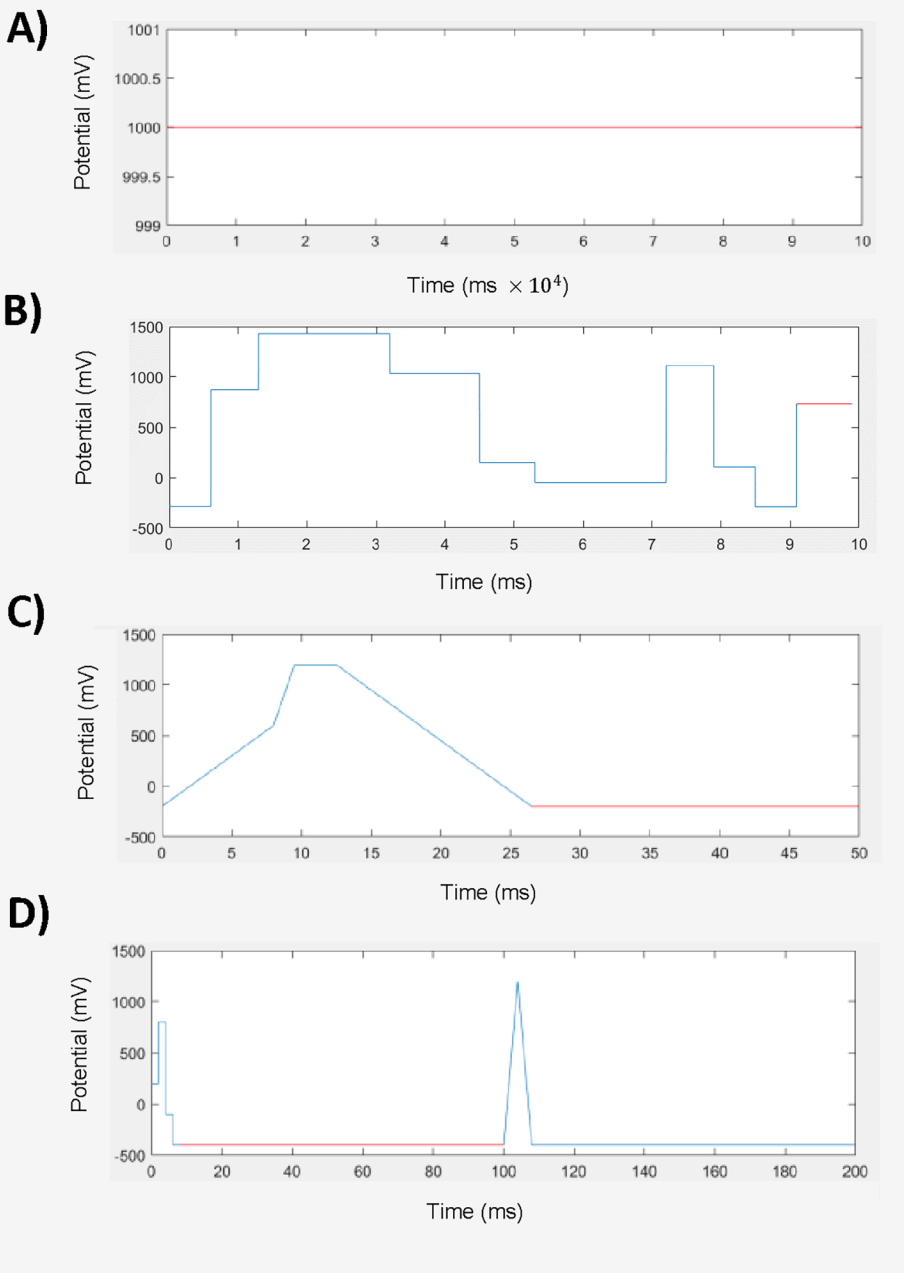

Figure 3. Examples of waveforms designed in SeroSignalGen. (A) Continuous hold waveform for static oxidation preconditioning, amperometric experiments, accumulation waveforms, *etc.* (B) Randomly generated pulse waveform without hold times, based on ref 59; custom tau, step, and hold times can be implemented. (C) Multiple-scan rate waveform, based on ref 7. (D) Dual alternating rapid pulse and fast scan waveform from ref 29.

acquisition and analysis.[29] Here, we provide a quick-start guide for users familiar with voltammetry and looking for an intuitive software solution with specific yet customizable capabilities. We envision the SeroWare package advancing acquisition techniques and data analysis tools across the voltammetry field. Future releases will incorporate streamlined chemometric processing (i.e., supervised machine learning regression for neurochemical concentration predictions) and community-accessible databases for voltammetry training data. To this end, we include tutorial coding notebooks on the import and machine learning analysis of SeroWare data in Python (SeroML), available at https://github.com/csmova/SeroML.

2. RESULTS & DISCUSSION

SeroWare is organized into three MATLAB modules that interact seamlessly and logically in a manner understandable by voltammetry users of different experience levels. The modules include SeroSignalGen, SeroAcq, and SeroDataProcess (Figure 1). Together, these modules handle waveform generation, data acquisition, and initial processing of raw data, respectively, along with external event control, filtering, analysis, and visualization tools.

2.1. SeroSignalGen. The SeroSignalGen module enables the creation and visualization of any voltammetry waveform in a versatile yet simple and user-friendly manner. The user can load a previously generated waveform as a *.sig* file or generate a new waveform to be saved (and shared) as a *.sig* file. The signal

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generation user interface and a fast-scan waveform commonly used for dopamine monitoring are shown in Figure 2.[57]

To generate a custom waveform, a user selects parameters such as waveform frequency, potential steps or scan rates, and hold times. Default waveform frequency values are provided as buttons for ease of use (*e.g.*, 10 Hz for *in vivo* measurements,[58] 60 Hz for *in vitro* preconditioning[31]). The user can also set custom frequencies within the limits of the hardware used. The sampling frequency (the frequency at which the data acquisition card samples measured data) can be set to common values (100 kHz or 250 kHz) or custom values using the text box. Faster sampling frequencies up to and exceeding 1 MHz are becoming more commonplace. They can be used with SeroSignalGen provided the hardware, including the acquisition card, supports these frequencies. Data files are generated in SeroAcq (*vide infra*), where users set the number of sampled points they want to retain in the data files (*e.g.*, data need not be retained during hold times for smaller data file sizes).

SeroWare can be used to build custom waveforms. The waveform file is built by vectorizing user-defined waveform "segments". These segments can be cathodic or anodic scans at user-defined scan rates, hold potentials, or pulse steps defined by hold times and the numbers of sampled points. Figure 3 shows four waveforms used in previous studies,[7,29,59] which can be quickly built, shared, and edited in the *.sig* file format using SeroSignalGen.

The characteristics of each waveform segment are displayed and automatically calculated. A segmented approach has several benefits: 1) segments can be easily reordered using the up/down/delete/add buttons in the segment table, and 2) users can build segments across any potential range by entering the desired amount of time or number of points to sample (for example, if a specific scan rate or a minimum number of sampled points is desired). Parameters are automatically updated as needed, and segments are visualized in real-time plots. Waveforms are named and saved. This feature allows the sharing and editing of waveforms across users, which is helpful given the increasing numbers and complexity of recently published waveforms.[4,5,7,8,19,20,60] Multiple waveforms can be concatenated to facilitate comparing waveform performance.[29] Unique data handling procedures for combined waveforms are also available (see Methods). Users can load and edit a previously generated *.sig* file using the load signal button. Table 1 summarizes SeroWare features described throughout the manuscript and compares them to previous voltammetry software reports.

2.2. SeroAcq. Users acquire voltammetry data by launching the SeroAcq module. A *.sig* file is loaded in SeroAcq. Global experiment parameters are set, including the preamplifier gain and data storage options. (See the User Guide in the Supporting Information for more information on establishing hardware communication). Once the acquisition has started, real-time data are visualized in a temporal plot of current vs. time at a user-defined voltage (*e.g.*, the oxidation potential of dopamine; Figure 4, top plot). This voltage can be set interactively during the acquisition, such that users can select various waveform voltages to monitor the current and the plot will update in real-time. Noise, drift, and other experimental factors at specific regions of interest can be straightforwardly monitored. Experimental events such as stimulations and injections can be labeled and time-stamped through the GUI. The visualization strategy includes cyclic voltammogram false-color plots (Figure 4). Additional data visualization options are available in a separate postacquisition module (see SeroDataProcess below).

Table 1. Comparison of Published Fast Voltammetry Software for Neurochemical Analyses[a]

	Demon	HDCV	SeroWare
open source	×	×	√
user Guide, tutorials, and videos freely available	×	×	√
waveform generation interface with shareable file format	×	√	√
real time data visualization	√	√	√
event labeling (e.g., timestamps)			
manual (user editable)	×	×	√
automated (device-controlled)	√	√	√
digital filters			
preset filters	√	√	√
custom digital filter builder interface	×	×	√
kinetic analyses	√	×	√
auxiliary equipment control(s)			
electrical stimulation	√	√	√
micromanipulator control	×	×	√
injector valve control	×	×	√
real-time waveform modification	×	×	√
single file format (i.e., events and voltammograms stored together)	×	×	√
figure generation and data reporting	√	√	√
optimized data and error handling	×	√	√
artifact removal	√	√	√
chemometric analyses	√	√	√*
automated peak finding	√	×	√*
multichannel electrodes/electrophysiology	×	√	√*

[a]An asterisk (*) denotes partial functionality, and/or upcoming or future releases. Note that due to multiple releases and/or the unavailability of other listed software, information for Demon, HDCV, or SeroWare may be out of date and rely only on reports at the time of writing and/or correspondence with the maintainers of the packages

2.2.1. Acquisition Modes. SeroAcq offers several features not previously available in other software. These include "Accumulation mode" and "Resting voltage mode", which can apply impromptu changes to a waveform during acquisition in real-time without requiring the experiment to be stopped or a new waveform to be loaded. For example, the accumulation mode interrupts the applied analytical waveform and holds the electrode at a constant potential to accumulate charged analytes at the surface for sensitivity enhancements. The Resting voltage mode allows the analytical waveform hold potential or "nonsampled" region to be modified. The software applies these changes in real time through design patterns such as event listeners, callback functions, and refresh cycles discussed in the *Methods* and Supporting Information. These modes are particularly interesting for advanced users developing new waveforms that want to test multiple waveforms or different hold potentials/times rapidly or otherwise perform adsorption-based experiments.[4,6−8,29,60] We note that impromptu waveform changes may induce electrode drift and other electrochemical artifacts due to various phenomena occurring at electrode surfaces.[61] Thus, these waveform augmentation features and resulting data should be used and interpreted cautiously. Allowing sufficient time for waveform conditioning may help to alleviate these

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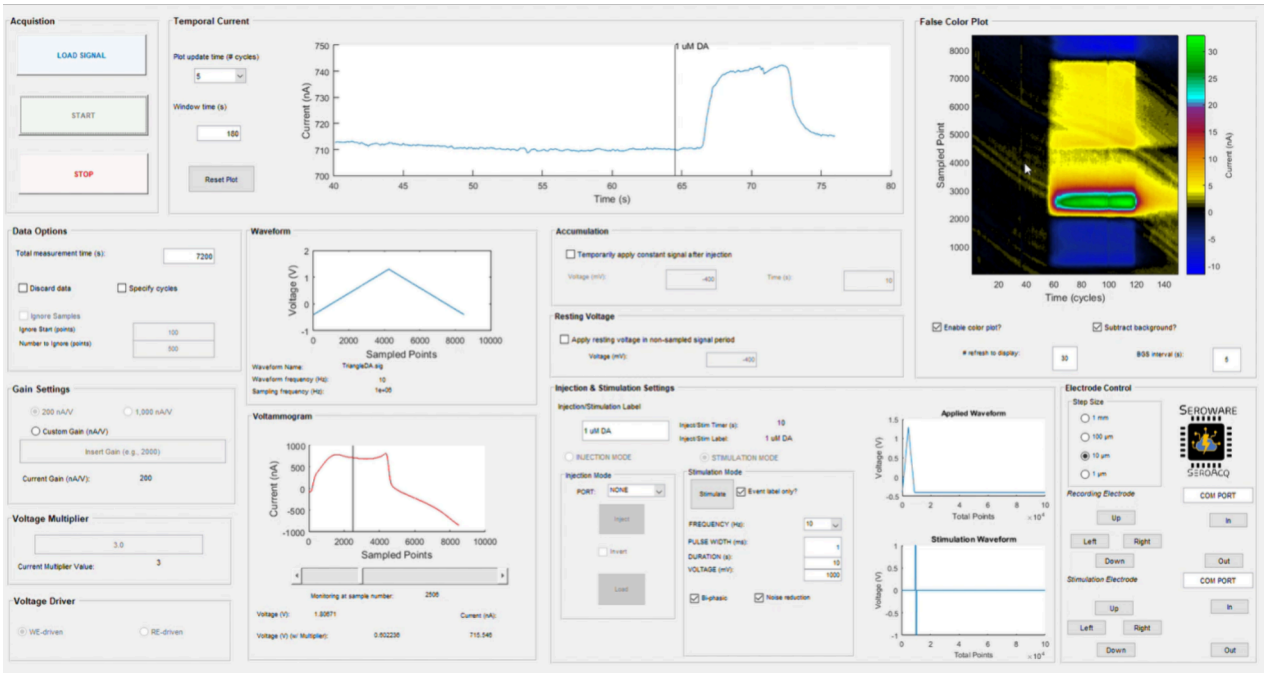

Figure 4. SeroAcq graphical user interface. A 1 μM injection of dopamine in artificial cerebrospinal fluid using a flow cell is shown. A triangle waveform is applied at a 7 μm carbon-fiber microelectrode vs a Ag/AgCl reference electrode. All data are nonbackground subtracted, except the false color plot (top right).

issues. More information, tutorial videos, and example data are found in the Supporting Information.

Experiments can be run in "Discard mode" if data do not need to be saved (*e.g.*, conditioning or equilibration experiments).[61] Discard mode does not save any of the data into a file but still allows control over the acquisition. Using "Ignore mode", any range of data points in a collected voltammogram can be ignored (not saved). Herein, "points" refers to sampled points, which are dictated by the sampling frequency and used to convert sampled points to time. For example, at a data density of 125 kHz, a sampled point is acquired every 8 μs. Thus, an 8 ms waveform contains 1,000 points. As another example, using dual alternating rapid pulse and fast scan waveforms (Figure 3d), points 1,001−11,500 can be discarded (this is the region of constant hold voltage, which is unnecessary for analysis).[29] In this scenario, of 12,500 total sampled points, only the first and last 1,000 points were needed for analysis. Thus, data acquisition was run in Ignore mode, with the ignore start point at 1,001 and the number of sampled points to ignore as 10,500. This practice considerably reduces file sizes and data overhead, particularly for long (hours) *in vivo* experiments. Notably, Ignore mode does not affect the waveform being applied; all potentials are still applied as dictated by the waveform *.sig* file. Certain user-defined portions of the resulting voltammograms are just not saved.

Other acquisition modes include "Injection mode" and "Stimulation mode". The injection mode is commonly used during *in vitro* experiments where calibration/training data are collected using a multiport valve and a flow cell. The Stimulation mode refers most widely to an *ex vivo* or *in vivo* experiment involving evoked release (*e.g.*, pharmacologic, optogenetic, electrical, or behavioral/environmental stimulation). SeroWare offers several controls to administer pulse trains for electrical stimulation. Stimulation waveforms can be built in real-time during data acquisition (Figure 4). To ensure maximal flexibility, users can run the Stimulation mode to apply event markers manually for devices that do not communicate directly with SeroWare. Event markers are time stamps generated automatically by the software to indicate when an experimental event of interest has occurred.

Thus, SeroWare includes exemplary code and tutorials for those wishing to establish communication with auxiliary devices for direct control, such as injectors and stimulating electrodes. Manual event marking enables an "out of the box" workaround for users wanting to use the acquisition and analysis capabilities of SeroWare immediately. External events can be generated without forcing communication with auxiliary hardware/software. Timestamps are automatically labeled and preserved when the data are analyzed and exported (see below).

2.2.2. Auxiliary Equipment Control. SeroAcq offers optional control for positioning recording electrodes. This type of device will automatically be recognized and listed as a configuration option for users having COM port communication with a micromanipulator controller. Users select the step size at which to (re)position electrode(s) and the direction(s) in which to move. We tested the software control with a Sutter Instruments MPC/ROE 200 micromanipulator controller. We provide the control code within the source code (see User Guide in Supporting Information). Due to the various types of instrumentation used in combination with potentiostats, users may need to configure additional devices (see User Guide in Supporting Information). Requests for or issues with connecting devices can be submitted via GitHub for community feedback.

2.3. SeroDataProcess. Once data acquisition is complete, saved *.dat* files can be visualized and analyzed in the SeroDataProcess module, which has a main module and two submodules (Figure 5). The main module is SeroProcessData.

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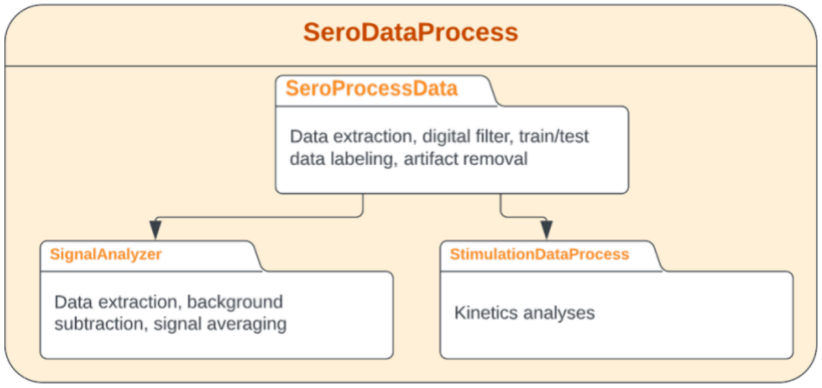

Figure 5. SeroDataProcess module and submodules.

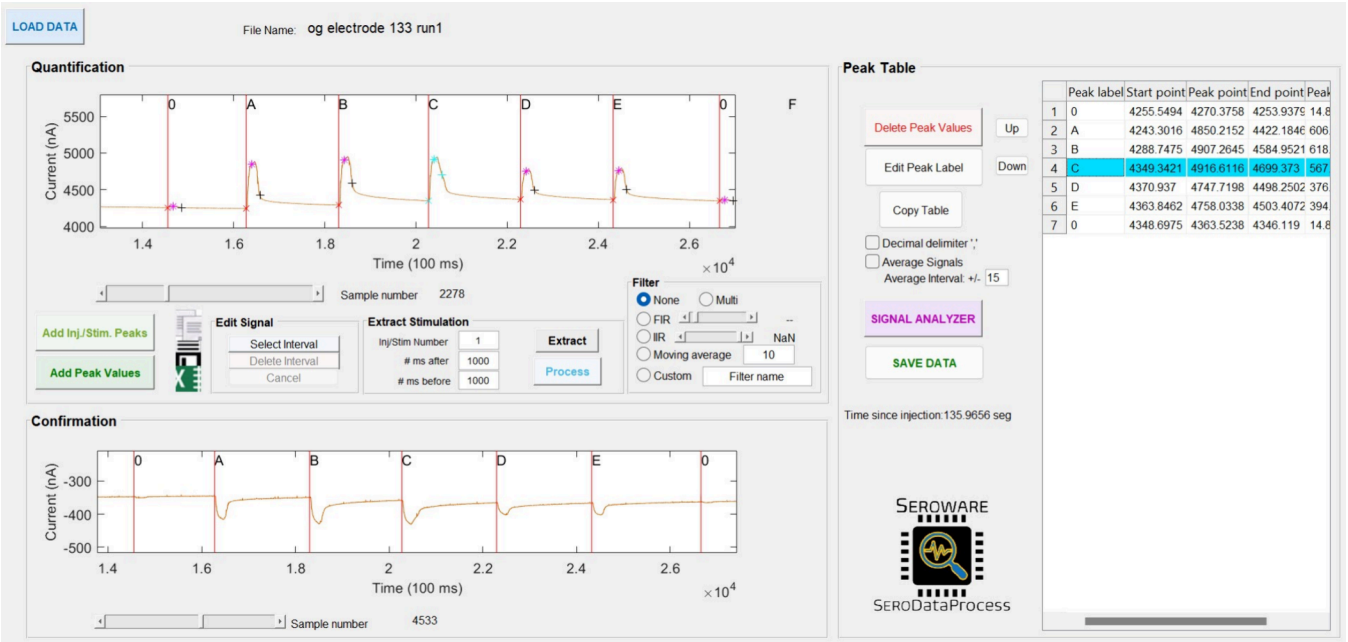

Figure 6. SeroDataProcess interface. A flow-cell experiment for injections of various concentrations of serotonin and dopamine in artificial cerebrospinal fluid is shown. Data were collected using a rapid pulse waveform (ref 29) applied to a 7 μm carbon-fiber microelectrode vs a Ag/AgCl reference electrode. The top panel shows data from the anodic segment of the pulse (+0.8 V), while the bottom panel shows data from the cathodic segment of the pulse (−0.1 V). Red lines indicate injection markers annotated during data acquisition. The colored dots (upper panel) represent user-defined analysis time points (see the user guide). All data are nonbackground subtracted.

Current vs time data are automatically plotted in the "Quantification" panel at voltage and point frequencies specified during acquisition. Events (i.e., injections, stimulations) are automatically labeled and time-stamped (Figure 6, **top**). Users can define areas of the data to extract for further analysis based on event markers. Alternatively, they can add and label such regions manually. Another temporal current plot is autopopulated in the "Confirmation" panel at a second user-defined voltage (Figure 6, **bottom**). We have found that visualizing two current−time traces at different voltages is helpful during waveform development or *in vivo* analyses to identify data regions to extract for subsequent analysis (*e.g.,* areas defined by anodic and cathodic peaks).

Users can individually extract identified peaks using the Peak Extraction panel. Extracting peaks enables users to run kinetic analyses of stimulation and uptake data (see *StimulationDataProcess*). Data can be plotted in new windows, exported, and saved in various ways. Artifact removal can be performed using the select and delete interval buttons. In addition to moving and constantly updated color plots generated in SeroAcq, static color plots can be automatically generated in SeroDataProcess at user-defined intervals for postacquisition analysis or to produce figures (see SignalAnalyzer below).

Users can save analysis files (extracted data) at any point to avoid losing progress or data on peak identification when work needs to be interrupted. For example, users analyzing long experiments (*i.e.*, hours) can stop and return to a data file as needed. They can also save and share analyzed files with others in a reproducible and documented manner. Unlike previous software packages, SeroWare can acquire, timestamp, and examine the entirety of multiple hours-long experiments in a single session.[24]

Several preset digital filtering options are available, including a moving average filter, a published infinite impulse response (IIR) filter developed for voltammetry baseline detrending,[16] and a new finite impulse response (FIR) filter we created. Further, SeroWare is fully incorporated with the MATLAB Filter Builder GUI. Users can choose a custom filter option in

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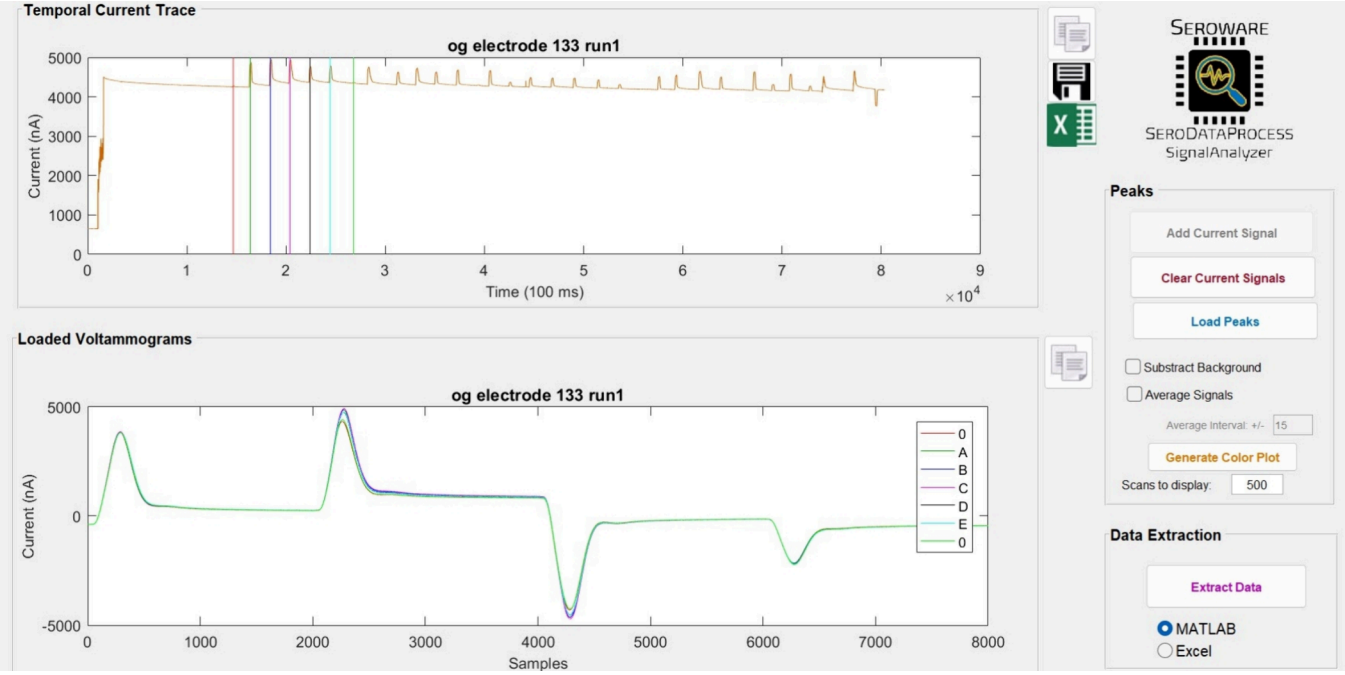

Figure 7. SignalAnalyzer GUI submodule for SeroDataProcess. The top panel shows the expanded current−time trace shown in the top panel of Figure 6. The bottom panel shows representative, nonbackground subtracted voltammograms for each trace, defined by the purple stars in Figure 6.

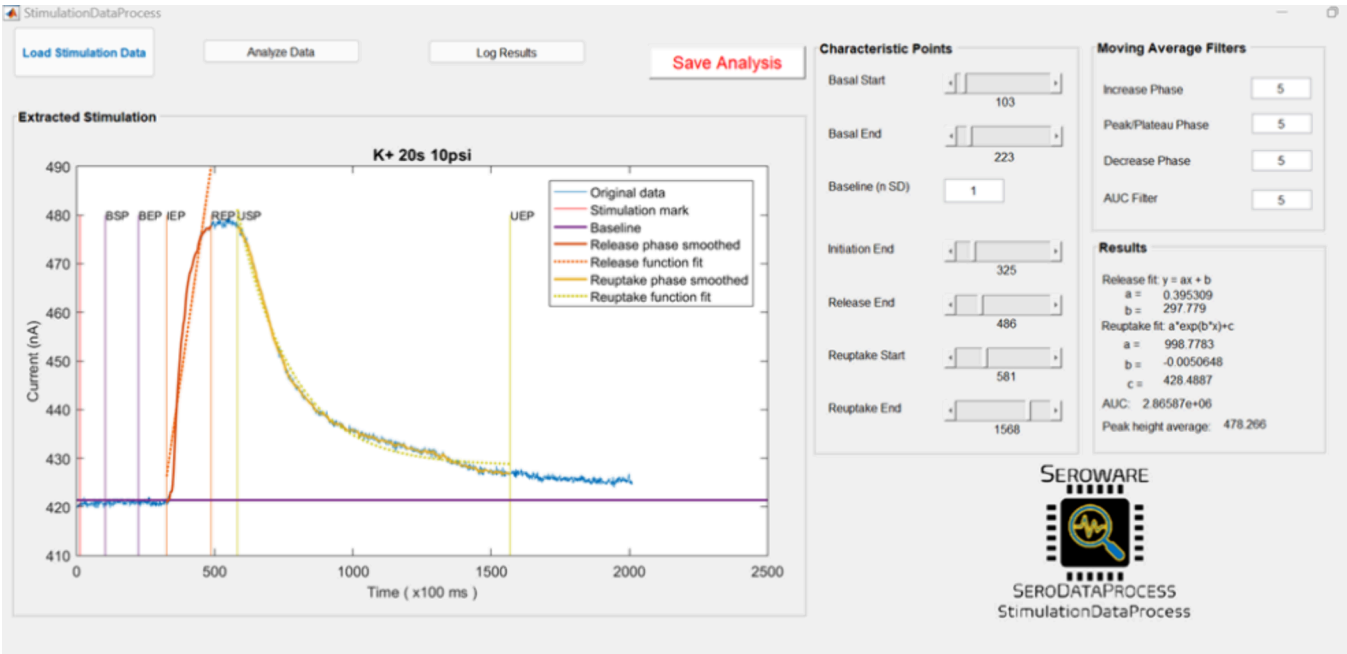

Figure 8. StimulationDataProcess GUI submodule of SeroDataProcess. BSP and BEP = basal start and basal end points; IEP = initiation end point; REP = release end point; USP and UEP = reuptake start and end points, respectively. Data were collected from the dorsal striatum of a mouse. Using a picospritzer set to a 20 s pressure ejection at 10 psi, artificial cerebrospinal fluid containing 120 mM KCl was applied adjacent to the recording electrode (7 um carbon-fiber microelectrode vs Ag/AgCl), using the waveform from ref 29.

SeroDataProcess from over a dozen digital filter design options and specifications to visualize frequency responses (see Supporting Information). When users are satisfied with the data filter choice, standard or custom filters are immediately applied to the voltammetry data loaded by the user and visualized in the plots. Together with the signal processing tools in MATLAB, SeroWare enables the incorporation of new, custom filters regardless of whether a user has a filter already programmed in MATLAB. Users can save and share their filters for reproducibility. Incorporating powerful MATLAB analysis toolboxes with the SeroWare environment seamlessly provides a key advantage over LabVIEW software. Data can be extracted in filtered or raw formats using the SignalAnalyzer submodule, accessible by clicking a single button.

2.3.1. SignalAnalyzer. The ease, speed, and versatility at which SeroWare offers data extraction is a significant

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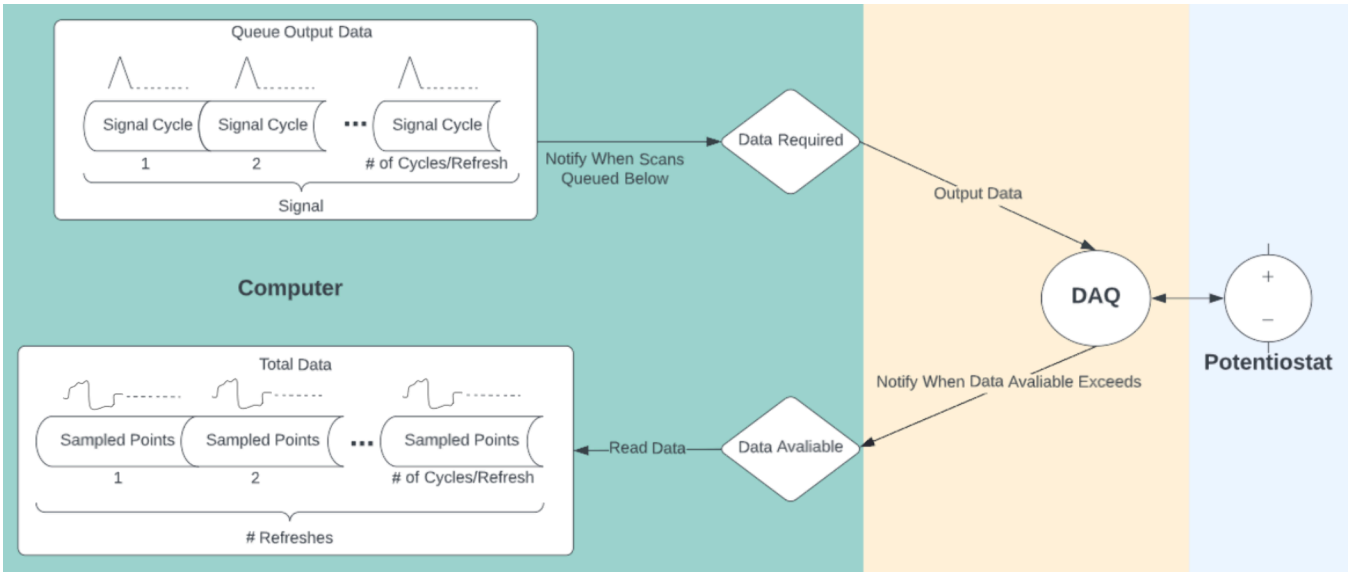

Figure 9. SeroAcq data flow.

advantage, especially as data wrangling (i.e., the process of transforming data into another format for a specified task) for various analysis pipelines can be cumbersome.[62] To begin extracting processed data, a separate tab is opened via SignalAnalyzer (Figure 7). A single button click loads the selected data from SeroDataProcess. It allows users to visualize their voltammograms in unraveled, averaged, background subtracted, and color-plotted formats.

Several options exist for data extraction to fit users' needs and data limits. The ease and versatility of SeroWare in automating data exporting are other key software benefits. Data can automatically be parsed and labeled as desired before exporting to a *.mat* or *.xlsx* file; each peak is referenced to a label for splitting into machine learning training and validation sets. Statistical learning techniques continue to be adapted for voltammetry.[11,13,29,30,63−74] SeroWare was designed with these techniques in mind to streamline data from waveform to machine learning model.

2.3.2. StimulationDataProcess. An analysis strategy for *in vivo* voltammetry involving neurotransmitter monitoring is fitting data to kinetic models of release and uptake.[75] To fit a kinetic model to an electrical stimulation event, SeroWare provides an extraction and analysis procedure (Figure 8). In this initial release, SeroWare fits data to uptake models using exponential decay rather than Michaelis−Menten models documented elsewhere.[27] Users can incorporate Michaelis−Menten and other kinetic models into future releases. Nonetheless, parameters associated with exponential decay models have been shown to correlate well with Michaelis−Menten parameters and do not require the saturated uptake conditions needed for Michaelis−Menten curve fitting.[24] Data can be extracted seamlessly into a separate file and immediately opened and analyzed in StimulationDataProcess by hitting the Extract and Process buttons in SeroDataProcess. Data shown in Figure 8 are from a potassium stimulation using an externally controlled picospritzer and the SeroWare event labeling feature.

CONCLUSIONS AND PROSPECTS

We present an open-source, thoroughly documented, customizable, yet user-friendly software for controlling, acquiring, and analyzing voltammetry data. The minimal hardware needed includes a potentiostat connected to a suitable computer with a National Instruments data acquisition card, a preamplifier, and appropriate electrodes. The software is compiled into a standalone version so that users without MATLAB licenses can run SeroWare at no cost. While we have developed SeroWare with neurochemistry applications in mind, this software can be used for virtually any type of voltammetry experiment. Other examples include electronic tongue[55] and amperometric detection,[76] which detect compounds ranging from amino acids and pharmaceuticals to pollutants, explosives, and food, and beverage components. The SeroDataProcess module can analyze and extract other multidimensional data types outside of voltammetry, provided they are formatted in MATLAB. SeroWare offers new acquisition and analysis capabilities, emphasizing reproducible results and community-built features.

SeroWare was purpose-built for user customization and sharing with the community at large. It is licensed under GNU LGPL 3.0 to ensure this remains the case. We wrote SeroWare specifically to be intuitive for users with different levels of voltammetry experience. For example, we beta-tested SeroWare with novice undergraduate student researchers in our group (see https://github.com/csmova/SeroWare). Importantly, we also designed SeroWare for advanced users who desire custom solutions. The User Guide provides extensive information on editing and adding to the SeroWare codebase. Users can edit the GUI using a code-free development environment (GUIDE). More in-depth documentation is provided for users wanting more extensive changes to the codebase (see Supporting Information).

Currently, SeroWare only supports NI card data acquisition and a handful of external devices. SeroWare does not support multichannel or array-based measurements at present. Depending on demand and open-source contributions, future releases may extend support to a broader array of vendors, multiplexed hardware setups, and additional analysis tools. Work is

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underway to incorporate further modules into SeroWare for seamless machine learning and database communication. We invite the community to contribute issues and pull requests via GitHub.

METHODS

Software. All software was written in MATLAB R2016a (MathWorks, Inc., Natick, MA). The reasons for choosing R2016a are detailed in the User Guide. In short, we recommend that users with MATLAB licenses download R2016a to run SeroWare, following the instructions in the User Guide. The compiled versions of SeroWare can be run in standalone mode, so no MATLAB installation or license is required. A MATLAB license is needed to make custom edits to the code. Users can choose between stand-alone versions of each module that launch the ready-to-use program in a single click or the raw MATLAB files, which provide straightforward access to implementing code modifications and executing changes in real time. Each module is written in an event-driven, function-based manner, such that various functions run and accept user inputs through interactions with graphical user interfaces (GUIs) in the form of callbacks, handles, and global scope variables (see the Supporting Information).

Data Flow and Storage. SeroAcq handles continuous acquisition over various lengths of time in a single file (i.e., seconds to several hours), even at maximum sampling rates where data files contain several gigabytes of data. This is facilitated by a "batching" strategy for reading and writing data to and from the DAQ card and computer (Figure 9). Briefly, SeroWare utilizes an object-oriented approach to events and listeners, combined with the built-in MATLAB Data Acquisition Toolbox. Once an acquisition session is started, the software prepares a "batch" of waveform cycles (i.e., the repeating voltage train to apply). It initializes a matrix of the expected size of the voltammogram data to be collected during a batch. As the DAQ card nears the end of a batch of waveform cycles and the data matrix is populated, the software sends the next round of waveform cycles to the card and reads the data from the DAQ card to computer memory.

Users can configure how often data acquisition buffers are read or written based on computer performance by adjusting the plot update time (and thus, number of refresh cycles). This feature allows users to conserve computer processing power as needed by selecting higher values of plot update times. Users can define desired measurement times for continual data acquisition before stopping automatically or can stop the acquisition manually at any point. Data are saved in a *.dat* format. The data batching procedure allows the software to employ versatile error-handling routines to save data even if acquisition errors occur. This waveform batching and queuing procedure also enables *ad hoc* modification of waveforms in the accumulation/resting voltage modes described above.

Hardware. A Pine WaveNeuro Single Channel potentiostat with a 200 nA/V or 1,000 nA/V headstage (Pine Research, Durham, NC) and an NI PCIe-6363 card (National Instruments (NI), Austin, TX) were used for data acquisition. A 64-bit Dell Precision 3650 Tower with 32 GB RAM and an Intel i7−11700 processor were used to run the software and for data acquisition and processing. SeroWare was also tested using an EI-400 potentiostat (Cypress System, USA), a custom headstage, and a PCI-6221 card. Because SeroWare was not written to be compatible with specific hardware, only a few configuration steps were needed to switch between hardware configurations. A DS4 Biphasic Stimulus Isolator (Digitimer, Letchworth Garden City, UK) was used to test the electrical stimulation capabilities of the hardware. An MPC 200 controller and ROE-200 system (Sutter Instruments, Novato, CA) were used to test the external control of a micromanipulator. Two E60 and A60 6-port valves (VICI Valco Instruments, Houston, TX) and a flow cell (Pine Research) were used to test the control of external devices for *in vitro* injections.

We wrote the software to be straightforwardly compatible with standard hardware and other external devices used during voltammetry experiments. For each, we provide working and example code that can be modified for user needs, regardless of specific hardware or connections. The hardware described above can be a starting point for new users. However, SeroWare can be modified to be compatible with other hardware as users dictate depending on the density of data acquired and other tasks that must be run by (a) computer(s). If specified before data acquisition, working-driven or reference-driven electrode setup can be used with SeroWare; for example, Pine potentiostats offer working-electrode-driven head stage amplifiers, but this can vary by manufacturer.

ASSOCIATED CONTENT

Data Availability Statement

All data and code presented in this paper are available on GitHub at https://github.com/csmova/SeroWare with corresponding installation instructions and User Guides. Linking to GitHub will make users aware of new releases and patches. For the most up-to-date user information and tutorial videos, readers are referred to GitHub (https://github.com/csmova/SeroWare). A direct link to the video tutorials can be found at https://www.youtube.com/playlist?list=PLdbCZpokXI1U-foYORhLEAdv8dZZEVf3b.

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acschemneuro.4c00799.

User guide (PDF)

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Author Contributions

M.A.F. designed and wrote the initial software. R.I. and C.S.M. wrote additional code and added features to each module. M.E.C. and M.E.W. assisted with testing the software and making tutorial videos. A.M.A. and M.A.F. guided the project. All authors wrote and approved the manuscript.

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Notes

The authors declare no competing financial interest.

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